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Research Article

Prunus zhuxiensis (Rosaceae), a new species from Hubei, China

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Abstract

In the present paper, we describe a new species, *Prunus zhuxiensis* (*P.* subg. *Cerasus*), from Hubei, China, based on long-term field observations. This species closely resembles *P. serrulata* in having corymbose-racemose or subumbellate inflorescences, hairy petiole, pedicel, involucral bracts and black drupes. However, *P. zhuxiensis* differs distinctly from *P. serrulata* by its sweet edible drupes (versus bitter, inedible drupes in *P. serrulata*), stipules 4-lobed at the base (versus linear stipules in *P. serrulata*), smaller bracts, shorter pedicels and styles pilose at the base (versus glabrous styles in *P. serrulata*). Furthermore, molecular phylogenetic analyses indicate that *P. zhuxiensis* and *P. serrulata* are placed in separate clades, supporting their distinction.

Key words: China, Hubei, *Prunus zhuxiensis*, taxonomy

Introduction

Shi et al. (2013) re-defined the infrageneric relationships of *Prunus* L., based on molecular phylogenetic analyses. Currently, about 65 species are recognized within *P.* subg. *Cerasus* (Mill.) A.Gray, of which 44 species occur in China (Su et al. 2021; Yi et al. 2024b). Some new species within this subgenus have been reported from China in recent years (e.g. Xu et al. (2022); Liang et al. (2023); Yi et al. (2024a)). However, the phylogeny of *Prunus* subg. *Cerasus* inferred from chloroplast and/or nuclear genomic data (Hodel et al. 2021; Shen et al. 2023; Su et al. 2023) only partially corresponds with previously proposed morphological sectional classifications (Yu and Li 1986; Wang 2014) and several cases have also been detected in other lineages of Rosaceae, including the tribe Maleae (Liu et al. 2019, 2020, 2022, 2023; Jin et al. 2023, 2024; Wang et al. 2024) and the tribe Potentilleae (Xue et al. 2023).

During a botanical expedition conducted a few years ago in Zhuxi, Hubei, China, we encountered an interesting species of *Prunus* subg. *Cerasus*. After careful and detailed observations, we concluded that it represents a species new to botanical sciences, which we formally describe herein.

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Materials and methods

We collected specimens and took pictures of the new species in Zhuxi, Hubei, China. The specimens of the new species were deposited at the Herbarium of Wuhan Botanical Garden, CAS (HIB) and PE (China National Herbarium). We also checked the specimens at HIB, PE and CVH (Chinese Virtual Herbarium, https://www.cvh.ac.cn/) of *Prunus* subg. *Cerasus*. We carried out morphological comparisons in the field and herbaria. The specimens were observed with dissecting microscopes.

The complete chloroplast genome of the new species *Prunus zhuxiensis* (GenBank accession number: PV208095) was assembled using Getorganelle 1.7.7.0 (Jin et al. 2020) with Illumina genomic DNA sequencing data. We also downloaded chloroplast genomes of other *Prunus* species and two outgroup species (*Malus domestica* (Suckow) Borkh. and *Spiraea martini* H.Lév.). Before constructing phylogenetic trees, the chloroplast genomes were aligned with MAFFT 7.520 (Rozewicki et al. 2019) and the alignment was trimmed with Gblocks (Talavera and Castresana 2007) in Phylosuit 1.2.3 (Zhang et al. 2020). The Maximum Likelihood (ML) phylogenetic trees were generated with IQ-TREE 2.2.0 (ultrafast bootstrap 10000 replicates) (Nguyen et al. 2015) in Phylosuit 1.2.3 (Zhang et al. 2020). The nucleotide substitution model was determined with ModelFinder 2.2.0 (Kalyaanamoorthy et al. 2017) in Phylosuit 1.2.3 (Zhang et al. 2020) and then Bayesian Inference (BI) was performed using MrBayes 3.2.7 (10,000,000 generations; Ronquist et al. (2012)).

Taxonomic treatment

Prunus zhuxiensis **Q.L.Gan, W.B.Xu & X.W.Li, sp. nov.**
urn:lsid:ipni.org:names:77360580-1
Figs 1–3

Diagnosis. *Prunus zhuxiensis* is similar to *P. serrulata* Lindl. (Li and Bartholomew 2003; Yi et al. 2024b) in its hairy pedicel and involucral bracts, corymbose-racemose or subumbellate inflorescences and black drupes, but the flowers of *P. zhuxiensis* appear before the leaves (at the same time as leaves in *P. serrulata*) and have reflexed sepals half as long as the hypanthium (spreading sepals up to as long as hypanthium in *P. serrulata*) and style pilose at the base (glabrous in *P. serrulata*), the fruits of *P. zhuxiensis* are sweet and edible, while those of *P. serrulata* bitter and inedible.

Type. China • Hubei Province, Zhuxi County, Quanxi Town, Baguashan Forest Farm, Hengduanshan, 32°3'50"N, 109°39'25"E, alt. 780 m, 15 March 2023, *Q.L. Gan 23-1-1* (***holotype*****:** HIB [barcode 0342513!]; ***Isotypes***, PE [barcodes 02553525!, 02553526!]).

Paratypes**:** • ibidem, alt. 780 m, 15 March 2023, *Q.L. Gan 23-1-2* (HIB [barcode 0346560!]), *Q.L. Gan 23-1-3* (HIB [barcode 0346559!]), *Q.L. Gan 23-1-4* (HIB [barcode 0346563!]); • ibidem, alt. 750 m, 26 April 2023, *Q.L. Gan 23-2-1* (HIB [barcode 0346561!]), *Q.L. Gan 23-2-2* (HIB [barcode 0346562!]), *Q.L. Gan 23-2-3* (HIB [barcode 0346564!]).

Description. Trees, deciduous, 8–12 m tall, bark grey, lenticels elliptic or long elliptic, sparsely transversely arranged. Young branchlets purple or green, densely grey pubescent. Leaf blades narrowly obovate, obovate or elliptic,

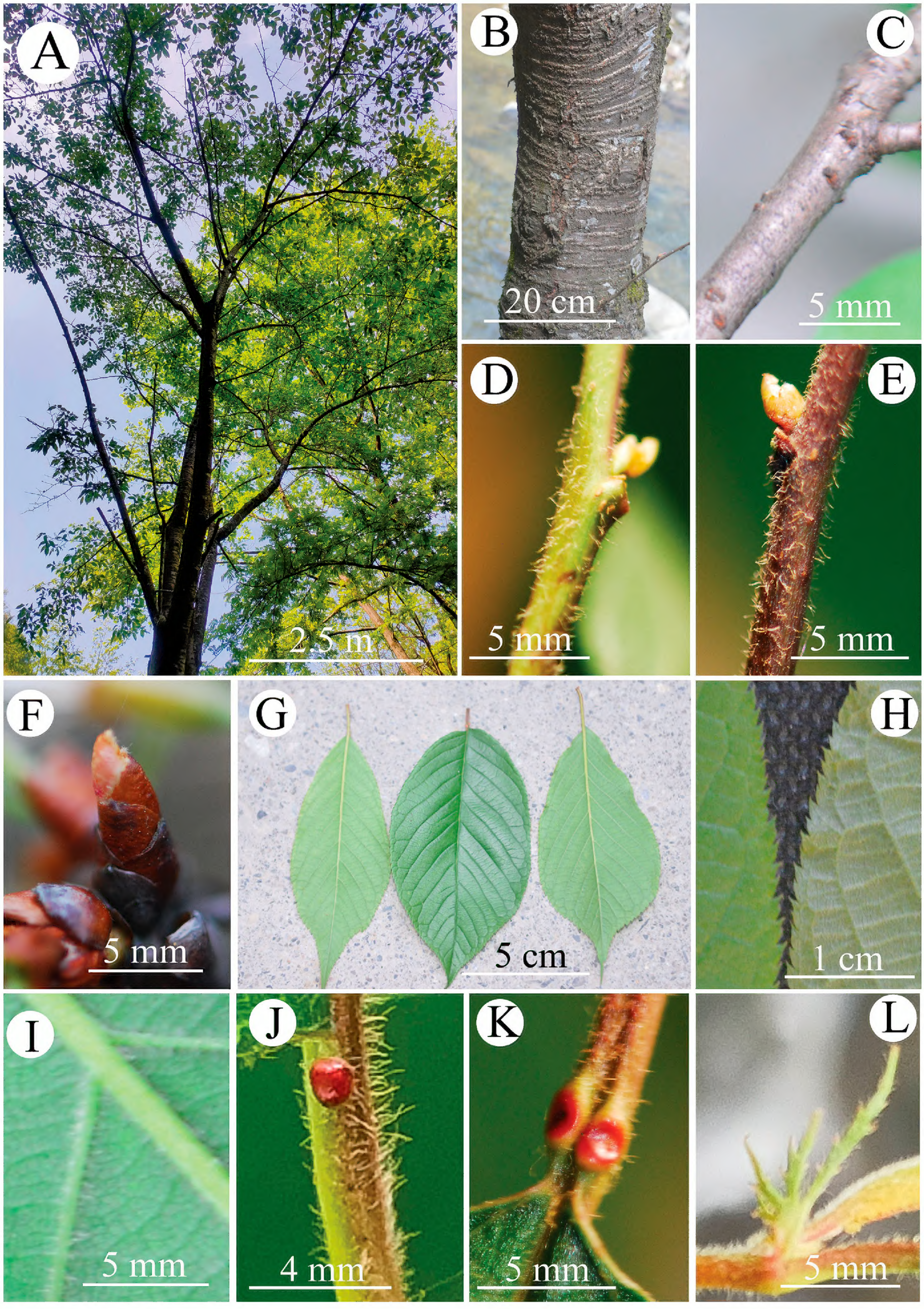

Figure 1. Vegetative characters of *P. zhuxiensis* **A** crown **B** trunk **C** old branch **D** branchlet **E** branchlet **F** winter bud **G** leaf blades **H** teeth at leaf margin **I** hairs on lower surface of a leaf **J** hairs on a petiole **K** glands at apex of a petiole **L** stipule.

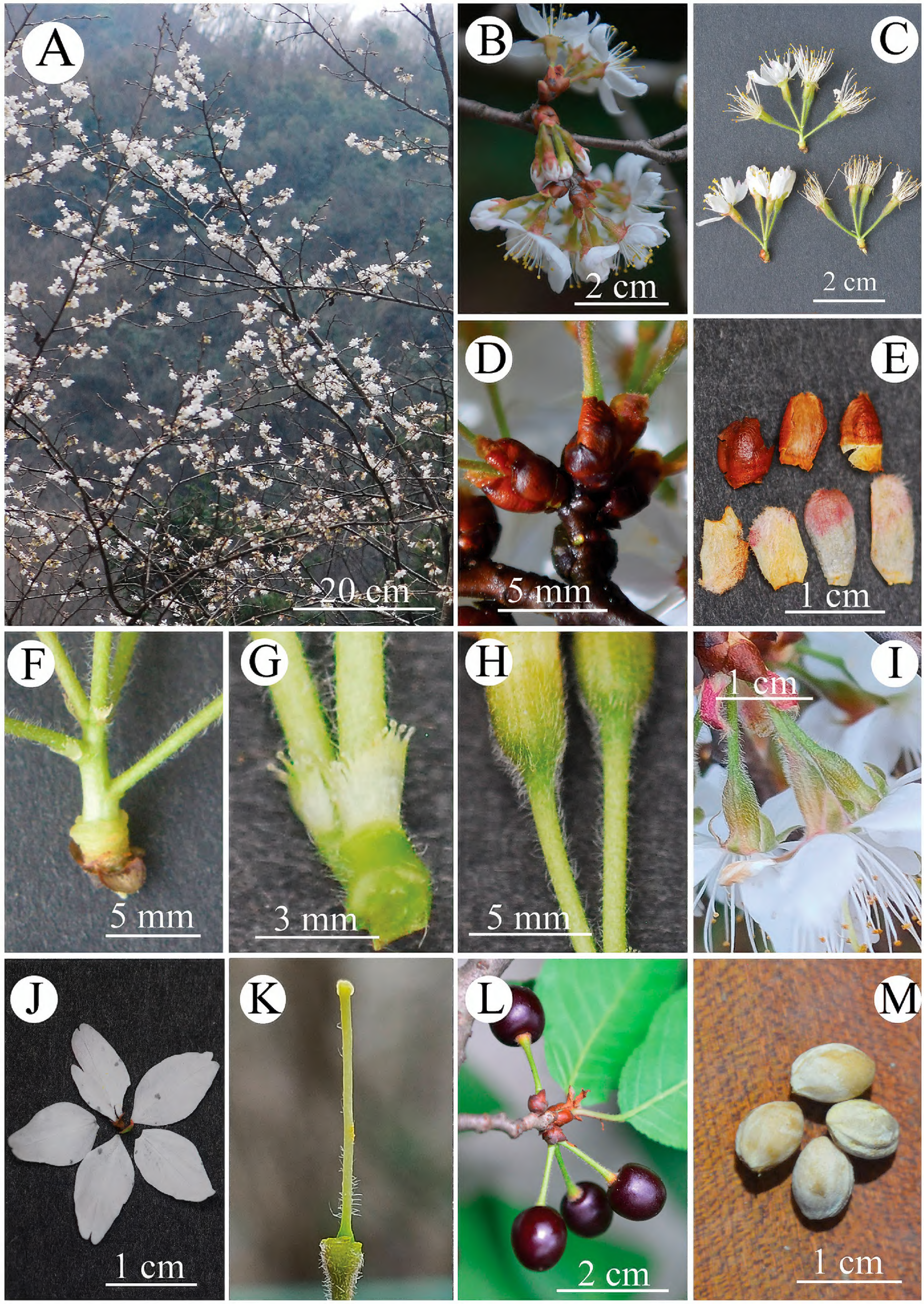

Figure 2. Reproductive characters of *P. zhuxiensis* **A** flowering branches **B** inflorescences **C** inflorescences **D** involucre **E** involucral bracts **F** peduncle **G** bracts **H** hypanthium **I** hypanthium and bracts **J** petals **K** ovary and style **L** drupes **M** endocarps.

Figure 3. The holotype of *P. zhuxiensis*.

3–12 × 1.5–5.5 cm, base cuneate or rounded, apex caudate or acuminate, margin crenately serrate or biserrate, teeth minute, tipped with apical glands, adaxially glabrous, abaxially white pilose on veins. Secondary veins 8–12 on

each side. Petiole 10–14 mm, pubescent, with two purple disciform glands at upper part. Stipules 4-lobed at base, lobes margin capitate gland tipped, laciniato-fimbriate. Flowers emerging before leaves. Involucral bracts ovate, oblong, 4–7 × 3.5–4.5 mm, densely pubescent adaxially. Inflorescences umbellate or corymbose-racemose, 3–5-flowered. Peduncles short or absent. Pedicel 7–12 mm, pubescent. Bracts greenish-white, obovate, 1.5–2.5 × 1.5–2.5 mm, conical glandular serrate at apex. Hypanthium tabulate or campanulate, 6–7 × 2–3 mm, pubescent abaxially. Sepals ovate-lanceolate, 2–3 × 0.8–1 mm, reflexed. Styles 12–13 mm, pilose at base. Petals ovate or narrowly ovate, white, 10–13 × 6–7 mm, bifid at apex. Stamens 38–44, filaments up to 12 mm. Drupes globose or ovoid, black, 8–9 mm long, sweet, edible. Endocarp flat ovoid, 7–8 mm long, smooth.

Phenology. Flowering in March, fruiting in May.

Distribution and habitat. *P. zhuxiensis* is distributed sparsely in the mixed evergreen and deciduous broad-leaved forest in the mountains or along streams at altitudes 600–1500 m around the type locality. The main accompanying species of *P. zhuxiensis* are *Salix wilsonii* Seemen ex Diels, *Sycopsis sinensis* Oliv., *Camellia cuspidata* (Kochs) H.J.Veitch, *Phoebe zhennan* S.K.Lee & F.N.Wei, *Juglans mandshurica* Maxim., *Albizia julibrissin* Durazz., *Pterocarya stenoptera* C.DC., *Cornus kousa* subsp. *chinensis* (Osborn) Q.Y.Xiang, *Photinia beauverdiana* C.K.Schneid etc.

Etymology. The specific epithet *"zhuxiensis"* refers to the type locality, Zhuxi, Hubei, China. The Chinese name of this species is Zhuxiyingtao (Pinyin).

Notes. *P. zhuxiensis* co-occurs with *P. serrulata* in the same plant community. They are similar in their hairy pedicel and involucral bracts and black drupes. However, these two species can be distinguished by the pilose style base of *P. zhuxiensis* (which is glabrous in *P. serrulata*) and the sweet and edible drupes of *P. zhuxiensis* (compared to the bitter and inedible drupes of *P. serrulata*). The morphological differences are shown in Table 1, Suppl. material 1.

Molecular phylogeny. Both the BI and ML molecular trees (Fig. 4, Suppl. material 2) demonstrate the monophyly of *Prunus* subg. *Cerasus*, which is consistent with Shen et al. (2023). Shen et al. (2023) split the subg. *Cerasus* into seven lineages (Clades IIIa–IIIg) and the species of each of these lineages also cluster together in our phylogenetic trees. The new species *P. zhuxiensis* does not group with *P. serrulata* and it is nested in clade IIIc of Shen et al. (2023) and sister to a subclade consisting of *P. dolichadenia* Cardot, *P. tatsienensis* Batalin,

Table 1. Morphological comparison between *P. zhuxiensis* and *P. serrulata* (Li and Bartholomew 2003; Yi et al. 2024b).

Characters	*P. zhuxiensis*	*P. serrulata*
Petiole	apex with 2 disciform glands	apex with 1–3 rounded glands
Stipule	4-lobed at base	linear
Secondary veins	8–12 pairs	6–8 pairs
Phenology (in Zhuxi County)	flowering in March	flowering in April and May
Pedicel	0.7–1.2 cm	1.5–2.5 cm
Hypanthium	green or slightly purple	dark purple
Sepals	reflexed, 2–3 mm long, about half as long as hypanthium	spreading, 5 mm long, nearly as long as hypanthium
Petals	ovate or narrowly ovate	obovate
Style	pilose at base	glabrous
Bracts	greenish-white, 1.5–2.5 × 1.5–2.5 mm	brown or tinged greenish-brown, 5–8 × 2.5–4 mm
Fruits	black, sweet, edible	black, bitter, inedible

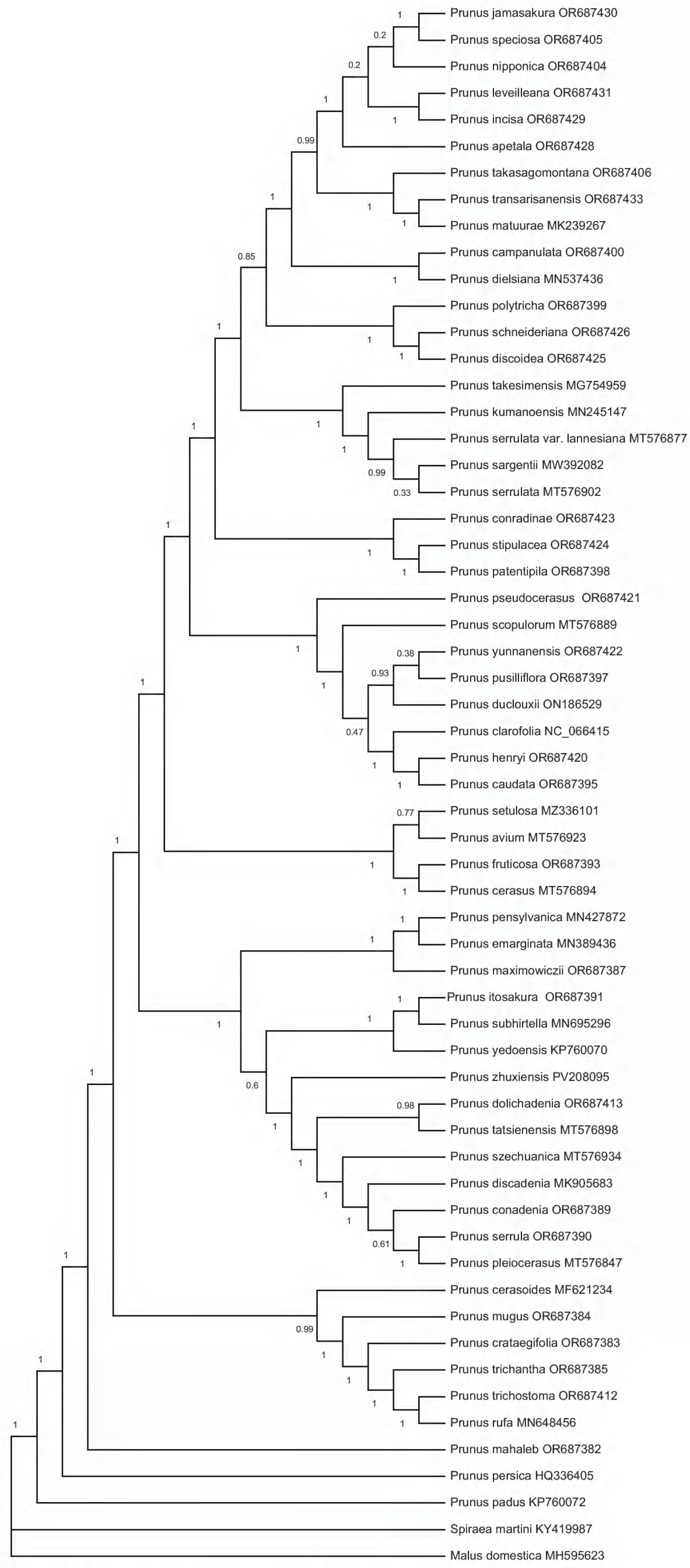

Figure 4. BI consensus tree of *Prunus* subg. *Cerasus*. GenBank accession number follows species name.

P. szechuanica Batalin, *P. discadenia* Koehne, *P. conadenia* Koehne, *P. serrula* Franch. and *P. pleiocerasus* Koehne. *P. serrulata* and *P. serrulata* var. *lannesiana* (Carrière) Makino and *P. sargentii* Rehder group together into a subclade as a part of clade IIIg of Shen et al. (2023). The present study shows that phylogenetic relatedness does not reflect the morphological resemblance of *P. zhuxiensis* and *P. serrulata*. While both *P. zhuxiensis* and *P. subhirtella* are placed in the same clade named IIIc of Shen et al. (2023), these two species share the characters of black drupes and hairy inflorescences and pilose style.

Key to species of *Prunus* subg. *Cerasus* in Zhuxi, Hubei, China (based on Li and Bartholomew (2003))

1a Bracts green, persistent **2**
2a Glands disciform or depressed at apex of teeth along bract margins **3**
3a Inflorescences subcorymbose-racemose or racemose ..... ***Prunus szechuanica***
3b Inflorescences umbellate..... ***Prunus tatsienensis***
2b Glands not disciform or depressed at apex of teeth along bract margins **4**
4a Bracts 5–20 mm; sepals spreading ..... ***Prunus setulosa***
4b Bracts 2–8 mm; sepals reflexed..... **5**
5a Hypanthium outside densely pilose ..... ***Prunus wangii***
5b Hypanthium outside glabrous **6**
6a Stamens 20–30; drupe long ellipsoid ..... ***Prunus clarofolia***
6b Stamens 32–54; drupe ovoid to subglobose..... ***Prunus conradinae***
1b Bracts brown or rarely greenish-white, rarely persistent..... **7**
7a Inflorescences more or less hairy or at least hairy when young **8**
8a Style glabrous **9**
9a Sepals about 1/2 as long as hypanthium ..... ***Prunus pseudocerasus***
9b Sepals about 2 times as long as hypanthium ..... ***Prunus dielsiana***
8b Style hairy..... **10**
10a Hypanthium tubular, base dilated..... ***Prunus subhirtella***
10b Hypanthium tabulate or campanulate, base not dilated ***Prunus zhuxiensis***
7b Inflorescences glabrous..... **11**
11a Sepals reflexed ..... ***Prunus cyclamina***
11b Sepals straight or spreading..... **12**
12a Leaf blade margin serrulate or biserrate with acuminate to aristate teeth ..... ***Prunus serrulata***
12b Leaf blade sharply serrate ..... ***Prunus conradinae***

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Author contributions

Xin-wei Li and Qi-liang Gan carried out field exploration, Qi-liang Gan took the pictures, Xin-wei Li and Wen-bin Xu wrote the manuscript.

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Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information, or NCBI (https://www.ncbi.nlm.nih.gov/).

References

Hodel R, Zimmer E, Wen J (2021) A phylogenomic approach resolves the backbone of *Prunus* (Rosaceae) and identifies signals of hybridization and allopolyploidy. Molecular Phylogenetics and Evolution 160: 107118. https://doi.org/10.1016/j.ympev.2021.107118

Jin JJ, Yu WB, Yang JB, Song Y, dePamphilis CW, Yi TS, Li DZ (2020) GetOrganelle: A fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biology 21: 241. https://doi.org/10.1186/s13059-020-02154-5

Jin ZT, Hodel RGJ, Ma DK, Wang H, Liu GN, Ren C, Ge BJ, Fan Q, Jin SH, Xu C, Wu J, Liu BB (2023) Nightmare or delight: Taxonomic circumscription meets reticulate evolution in the phylogenomic era. Molecular Phylogenetics and Evolution 189: 107914. https://doi.org/10.1016/j.ympev.2023.107914

Jin ZT, Ma DK, Liu GN, Hodel RGJ, Jiang Y, Ge BJ, Liao S, Duan L, Ren C, Xu C, Wu J, Liu BB (2024) Advancing *Pyrus* phylogeny: Deep genome skimming-based inference coupled with paralogy analysis yields a robust phylogenetic backbone and an updated infrageneric classification of the pear genus (Maleae, Rosaceae). Taxon 73(3): 784–799. https://doi.org/10.1002/tax.13163

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. Nature Methods 14: 587–589. https://doi.org/10.1038/nmeth.4285

Li CL, Bartholomew B (2003) *Cerasus* Miller. In: Wu ZY, Raven PH, Hong DY (Eds) Flora of China vol. 9. Science Press, Beijing & Missouri Botanical Garden Press, St. Louis, 404–420.

Liang SH, Qin B, Huang YH, Tang LM, Zhang ZJ, Li C, He YH, Jiang RH, Li JL (2023) *Prunus quanzhouensis*: A newly discovered species of *Prunus* subgen. *Cerasus* (Rosaceae) from northeastern Guangxi, China. Phytotaxa 622: 252–259. https://doi.org/10.11646/phytotaxa.622.4.2

Liu BB, Hong DY, Zhou SL, Xu C, Dong WP, Johnson G, Wen J (2019) Phylogenomic analyses of the *Photinia* complex support the recognition of a new genus *Phippsiomeles*

and the resurrection of a redefined *Stranvaesia* in Maleae (Rosaceae). Journal of Systematics and Evolution 57(6): 678–694. https://doi.org/10.1111/jse.12542

Liu BB, Campbell CS, Hong DY, Wen J (2020) Phylogenetic relationships and chloroplast capture in the *Amelanchier-Malacomeles-Peraphyllum* clade (Maleae, Rosaceae): Evidence from chloroplast genome and nuclear ribosomal DNA data using genome skimming. Molecular Phylogenetics and Evolution 147: 106784. https://doi.org/10.1016/j.ympev.2020.106784

Liu BB, Ren C, Kwak M, Hodel RGJ, Xu C, He J, Zhou WB, Huang C-H, Ma H, Qian GZ, Hong DY, Wen J (2022) Phylogenomic conflict analyses in the apple genus *Malus* s.l. reveal widespread hybridization and allopolyploidy driving diversification, with insights into the complex biogeographic history in the Northern Hemisphere. Journal of Integrative Plant Biology 64(5): 1020–1043. https://doi.org/10.1111/jipb.13246

Liu GN, Ma DK, Zhang Y, Hodel RGJ, Xie SY, Wang H, Jin ZT, Li FX, Jin SH, Zhao L, Xu C, Wei Y, Liu BB (2023) Phylogenomic analyses support a new infrageneric classification of *Pourthiaea* (Maleae, Rosaceae) using multiple inference methods and extensive taxon sampling. Taxon 72(6): 1285–1302. https://doi.org/10.1002/tax.13083

Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Molecular Biology and Evolution 32: 268–274. https://doi.org/10.1093/molbev/msu300

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Hohna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Rozewicki J, Li SL, Amada KM, Standley DM, Katoh K (2019) MAFFT-DASH: Integrated protein sequence and structural alignment. Nucleic Acids Research 47(1): 5–10. https://doi.org/10.1093/nar/gkz342

Shen X, Zong W, Li Y, Liu X, Zhuge F, Zhou Q, Zhou S, Jiang D (2023) Evolution of Cherries (*Prunus* Subgenus *Cerasus*) Based on Chloroplast Genomes. International Journal of Molecular Sciences 24: 15612. https://doi.org/10.3390/ijms242115612

Shi S, Li J, Sun J, Yu J, Zhou S (2013) Phylogeny and classification of *Prunus* sensu lato (Rosaceae). Journal of Integrative Plant Biology 55: 1069–1079. https://doi.org/10.1111/jipb.12095

Su N, Liu BB, Wang JR, Tong RC, Ren C, Chang ZY, Zhao L, Potter D, Wen J (2021) On the species delimitation of the *Maddenia* group of *Prunus* (Rosaceae): Evidence from plastome and nuclear sequences and morphology. Frontiers in Plant Science 12: 743643. https://doi.org/10.3389/fpls.2021.743643

Su N, Hodel R, Wang X, Wang JR, Xie SY, Gui CX, Zhang L, Yang C, Zhao L, Potter D, Wen J (2023) Molecular phylogeny and inflorescence evolution of *Prunus* (Rosaceae) based on RAD-seq and genome skimming analyses. Plant Diversity 45: 397–408. https://doi.org/10.1016/j.pld.2023.03.013

Talavera G, Castresana J (2007) Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. Systematic Biology 56: 564–577. https://doi.org/10.1080/10635150701472164

Wang XR (2014) An illustrated monograph of cherry cultivars in China. Science Press, Beijing.

Wang H, Li XY, Jiang Y, Jin ZT, Ma DK, Liu B, Xu C, Ge BJ, Wang T, Fan Q, Jin SH, Liu GN, Liu BB (2024) Refining the phylogeny and taxonomy of the apple tribe Maleae (Rosaceae): Insights from phylogenomic analyses of 563 plastomes and a taxonomic

synopsis of *Photinia* and its allies in the Old World. PhytoKeys 242: 161–227. https://doi.org/10.3897/phytokeys.242.117481

Xu SZ, Gan QL, Li ZY (2022) A new species of *Prunus* subgen. *Cerasus* from Central China. PhytoKeys 199: 1–7. https://doi.org/10.3897/phytokeys.199.84354

Xue T-T, Janssens SB, Liu B-B, Yu S-X (2023) Phylogenomic conflict analyses of the plastid and mitochondrial genomes via deep genome skimming highlight their independent evolutionary histories: A case study in the cinquefoil genus *Potentilla* sensu lato (Potentilleae, Rosaceae). Molecular Phylogenetics and Evolution 107956. https://doi.org/10.1016/j.ympev.2023.107956

Yi XG, Dong JJ, Chen J, Zhou HJ, Wu T, Gao SC, Chen XZ, Li M, Wang XR (2024a) Molecular and morphological evidence support a new species of Rosaceae *Prunus* subg. *Cerasus* from Wuyishan National Park, southeast China. PhytoKeys 237: 269–279. https://doi.org/10.3897/phytokeys.237.115098

Yi XG, Li M, Wang XR (2024b) A review on the taxonomy study of *Prunus* Subgen. *Cerasus* (Mill.) A. Gray. Journal of Nanjing Forestry University 48: 46–57.

Yu TT, Li CL (1986) *Cerasus*. In: Yu TT (Ed.) Flora Reipublicae Popularis Sinicae Vol. 38. Science Press, Beijing, 46–87.

Zhang D, Gao FL, Jakovlic I, Zou H, Zhang J, Li WX, Wang GT (2020) PhyloSuite: An integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Molecular Ecology Resources 20: 348–355. https://doi.org/10.1111/1755-0998.13096

Supplementary material 1

Comparison between *P. zhuxiensis* and *P. serrulata*

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Data type: jpg

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Supplementary material 2

ML consensus tree of *Prunus* subg. *Cerasus*

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Data type: jpg

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